

HUMAN TELOMERASE

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCGAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCCCGCCGCCCTCTCCGCCAGGTGTCTGCCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGCTGGACGGGGCCCGCGGGGCCCCCGAGGCCTTACCACCAGCGTGCGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCGCTCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCGCGCGCTGTACCAGCTCGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240

FIG. 1A

GGCGCTGCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGGGGTCTGGGCCCCACCCGGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCCATCCGTGGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCGGGTGTACGCGGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGAGCTGCTTGGGAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCTGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGCTGGTGCCCCAGGCCTCTGGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500

FIG. 1B

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GCCPAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGC GGGGCTGCGCTTGGCTG	1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
CGCAGGAGCCCAGGGGTTGGCTGTGTTCGGCCGAGAGCACCGTCTGCGTGAGGAGATC	1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC	1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTC	1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
TGGAGCAAGTTGCAAAGCATTGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGGGAG	1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA	1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCGGATTGTGAACATGGACTACGTCGTG	1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCSAGCGTCTCACCTCGAGGGTGAAGGCA	1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
CTGTTTCAGCGTGCTCAACTACGAGCGGGCGCGCGCCCGCCCTCCTGGGCGCCTCTGTG	2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAG	2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC	2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGC	2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAG	2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760

FIG. 1C

AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCAGATTCTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGCGGGATTGGCGGGAC LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	2580 860
GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCG GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	2640 880
AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	2700 900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAGGCTTTTGT ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	2760 920
CAGATGCCGGCCACGGCCTATTCCCCTGGTGGCGCCTGCTGCTGGATACCCGGACCCTG GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	2820 940
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	2880 960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCCGTGCGAACTCTTTGGGGTCTTGGCGCTG AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	2940 980
AAGTGTACAGCCTGTTTCTGGATTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	3000 1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	3060 1020

FIG. 1D

CGTTCG-334130

TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	1120
CCTGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTgatggccaccgcccacagccag	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132
Gccgagagcagacaccagcagccctgtcacgcccggctctacgtcccagggagggagggg	3480
Cggcccacaccagggcccgacccgctgggagtcctgaggcctgagtgagtggttgccgag	3540
gcctgcatgtccggctgaaggctgagtgccggctgaggcctgagcgagtgccagccaa	3600
gggctgagtggtccagcacacccgctgttccactccccacaggctggcgctcggtcca	3660
ccccagggccagcttttccctcaccaggagcccggttccactccccacataggaatagtc	3720
catccccagattcgccattgttcacccctcgccctgcccctcctttgccttccacccccac	3780
catccagggtggagaccctgagaaggacccctgggagctctgggaatttgagtgaccaaag	3840
gtgtgccctgtacacaggcgaggaccctgcacctggatgggggtccctgtgggtcaaatt	3900
ggggggaggtgctgtgggagtaaaatactgaatatatgagtttttcagttttgaaaaaaa	3960
aaaa	3964

FIG. 1E

FIG. 2

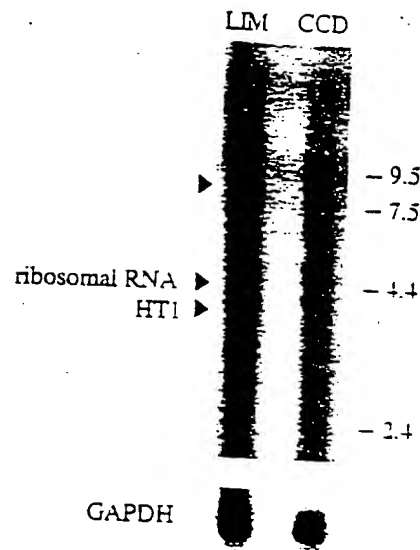


FIG. 3

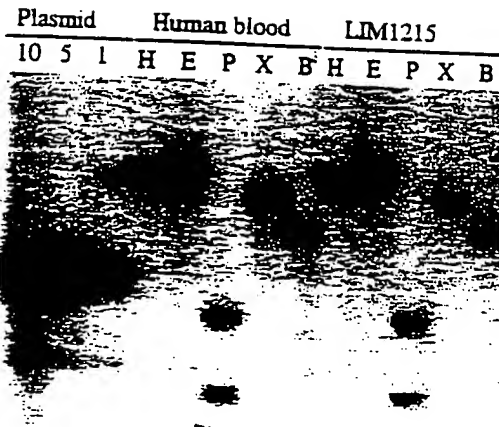


FIG. 4

a b c d e f g h i j k l m n o p

HT1

β -actin

FIG. 5

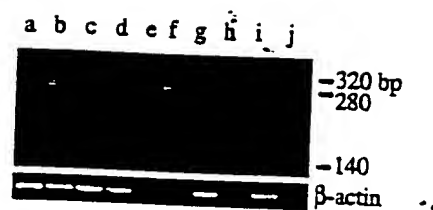


FIG. 6

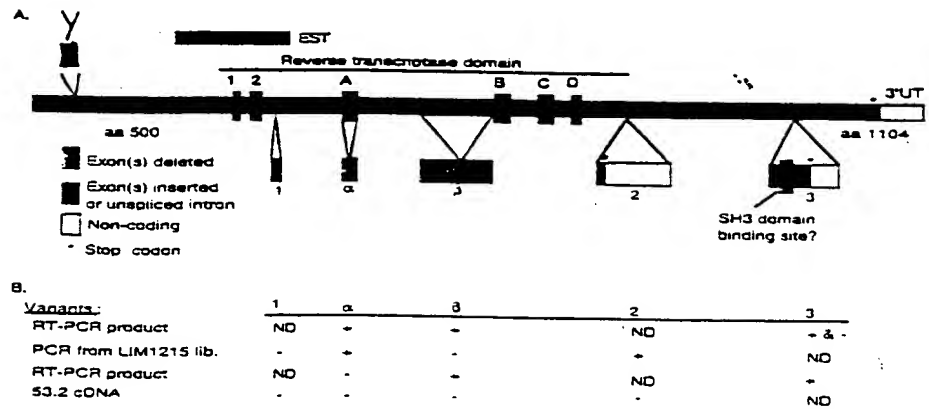


FIG. 7A and 7B

C

Figure 1 consists of 12 histograms arranged in a single row, labeled $k=1$ through $k=12$ from left to right. Each histogram shows the frequency of non-zero elements in the vector x_k . The x-axis for all histograms is labeled x_k and has tick marks at 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The y-axis is labeled 'count' and has tick marks at 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10. The distributions are roughly bell-shaped and centered around 5. The peak count (the number of times the value 5 appears) increases from 10 for $k=1$ to 10 for $k=12$. The distributions are very similar, with only minor variations in the tail counts.

FIG. 7C

05602193-104100

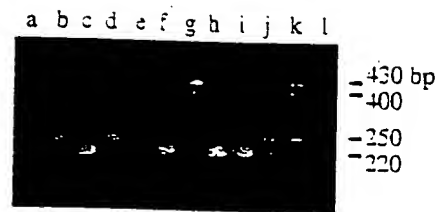


FIG. 8

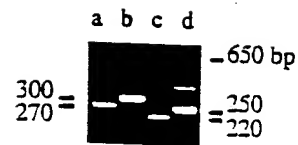


FIG. 9

sequence "Y" 104-105 bases

GGCCTCCCCGGGTCCGGCTCCGGCTGGGGTTGAGGGCGGCCGGGGGAACCAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases

GTGGCTGTGCTTTGGTTAACTTCCTTTTTTAACCAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases

GTGGATGTGACGGGCGCGTACGACACCATCCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTATCGAGCAGAGCTCCTCCCTG
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys

partial sequence "2" unknown length

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAG
Ter

GGCCGTTCGCTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT
CAGATGCCACAGGGTGGCCCTCGTCCCATCTGGGGCTGAGCACAATGCATCTTTCTG
TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTCTGTGCTATTTTGGTAA..

sequence "3" 159 bases

CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTCGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCCGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
GlyValGlyLeuGlyLeu *

FIG. 10A

_GACAGTCAACCAGGGGGGTTGACCGCCGGACTGGGCGTCCCCAGGGTTGACTATAGGA
 CCAGGTGTCCAGGTGCCTTGCAAGTAGAGGGGCTCTCAGAGGCGTCTGGCTGGCATGG
 GTGGACGTGGCCCCGGGCATGGCCTTCTGCGTGTGCTGCCGTGGGTGCCCTGAGCCCT
 CACTAGTGCCTGGGGGCTTGTGGCTTCCCGTAGCTTCCCCCTAGTCTGTTGTCTGG
 CTGAGCAAGCCTCCTGAGGGGCTCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)

```
GTGGCTGTGCTTTGGTTTAACCTTCCTTTTAAACAGAAGTCGGTTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGCCACGGGACACGCCAGGGGCCAT
GGCAGCGGCCCAACCCATTGTGCGCAGCTAGGTGGCCGAGGTGCCGTGCCTCCCA
GAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....
```

FIG. 10B

[illegible]

FIG. 11A

FIG. 11B

GTCCTACGTCGAGTC
V L R P V

FIG. 11C

Reference protein

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGAC	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGACCCGCGCGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGTCTGCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCGAGTGTCTGACAGGCGTGTGCSAGCGCGCGCGAAGAAGCTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCCGCGCTGTGGACGGGGCGCGGGGGCCCCCGAGGGCTTCACCACAGCGTGGCG	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCCAACACCGTGACCGACGCACTGCGGGGGAGCGGGGCTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCTGGGGCAGCAGCTGTGCTGCTGCTGCGCAGCTGCGCGCTCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCGAGCTGCGCTTACCAGGTGTGCGGGCGCGCGCTGTACAGCTCGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCGCGCGCGCGCGCACAGCTAGTGSACCGCGAAGCGCTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	200
CGGGCTTGAACCATAGCGTCAGGGAGGCGGGGTCCCGCTGGGCTGCCAGCCCCGGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGCGCGGGGCGAGTGCAGCGGAAGTCTGCGGTTGCCAAGAGGCGCGAGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
GGCGCTGCCCTGAGCGGAGCGGACGCGCGTTGGGCAAGGCTCTGCGCGCCACCGGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGCCTGGTTCCTGTGTGGTGTACCTGCCAGACCGCGCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTCTTTGGAGGGTCCGCTCTCTGGCACGCGCACTCCACCTATCCGTGGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACCGCGGGCGCGCGCATCCACATCGCGGCCACACCTCCCTGGGACACGCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCCGGTGTACGCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCGCTCCTTCTACTCAGCTCTCTGAGGCGCAGCGTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGGACTCCCGCAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCCAGCGCTACTGGCAAATGCGGCGCGTGTCTCTGGAGCTGCTTGGGAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGGCGCTACGCGGTGCTCCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420

FIG. 11D

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CCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAG 1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440

GAGGACACAGACCCCCGCTGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAG 1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460

GTGTACGGCTTCGTGCGGGCCTGCCTGCGCGGGCTGGTGGCCCCAGGCTCTGGGGCTCC 1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480

AGGCACAACGAACGCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT 1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500

GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGGGCTGCGCTTGGCTG 1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520

CGCAGGAGCCCCAGGGTTGGCTGTGTTCGGCCGAGAGCACCGTCTGCGTGAGGAGATC 1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540

CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTCGAGCTGCTCAGGTCTTTC 1680
LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560

TTTTATGTCACGGAGACCACGTTTCAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTG 1740
PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580

TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG 1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600

CTGTGGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCCGCTGCTGACGTCCAGA 1860
LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620

CTCCGCTTCATCCCAAGCCTGACGGGCTGCGGGGATTGTGAACATGGACTACGTCTGTG 1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640

GGAGCCAGAACGTTCCGCAGAGAAAAGAGGCCGAGCGTCTCACCTCAGGGTGAAGGCA 1980
GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660

CTGTTACGGTGTCTCAACTACGAGCGGGCGCGCGCCCGGCTCTGGGGCGCTCTGTG 2040
LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680

CTGGGCTGAGCATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAG 2100
LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700

GACCCGCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCTACACACCATC 2160
AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720

CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAACCCAGAACAGTACTGC 2220
ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740

GTGCGTCGGTATGCGGTGGTCCAGAAGCGCGCCATGGGCACGTCCGCAAGGCTTCAAG 2280
ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760

AGCCACGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGGCTCACCTG 2340
SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780

CAGGAGACCAGCCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG 2400
GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu 800

GCCAGCAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCCACACGCCCTGGCGCATC 2460
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820

AGGGGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG 2520
ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840

CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGGCGGGATTCGGCGGGAC 2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCG 2640

FIG. 11E

PRINT OF DRAWINGS
AS ORIGINALLY FILED

GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAAACCTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT	2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
CAGATGCCGGCCACGGCCTATTCCCTGGTGGCCTGCTGCTGGATACCCGGACCCCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	940
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTC	2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGCGGCTG	2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
AAGTGTACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGTTTCACGCATGTGTGCTGCAGTCCCA	3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGAGGGATGTGCTGGGGGCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACCTCAGGACAGCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132

FIG. 11F

FIG. 11G

[illegible]

FIG. 11I

ed protein that lacks me . A

[illegible]

FIG. 11J

[illegible]

FIG. 11K

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

FIG. 11L

[illegible]

FIG. 11M

[illegible]

FIG. 11N

ATGCCGCGGCTCCCGCTGCCGAGCGTGGCTCCCTGCTGCGCAGCCACTACCGCGAG 60
 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 GTGCTGCCGCTGGCCACGTTCTGTGCGGCGCTGGGGCCCGAGGGCTGGCGGCTGGTGCAG 120
 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
 CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTCGG 180
 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
 GACGCACGGCCGCCCGCCCGCCCGCTCCTTCGCGCAGGTG
 AspAlaArgProProProAlaAlaProSerPheArgGlnVal
 GGCCTCCCGGGGTCCGCTCCGCTGGGTTGAGGGCGGCTGGGGGAACAGCGACATCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCGCGCAGGTG
 G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
 TCCTGCCTGAAGGAGCTG 240
 SerCysLeuLysGluLeu 80
 GTGGCCCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAAGACGTGCTGSCCTTCGGC 300
 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
 TTCGCGCTGTGGACGGGGCCCGCGGGGGCCCCCGAGGGCTTCACCACAGCGTGCSC 360
 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg 120
 AGCTACCTGCCCAACACGGTGACCGACGCACTGCCGGGGAGCGGGCTGGGGGCTGCTG 420
 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140
 TTGCGCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCAGCTGCCGCTCTTTGTG 480
 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 CTGGTGGCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCGCTGTACAGCTCGGCGCT 540
 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 GCCACTCAGGCCCGCGCGCGCGCACGCTAGTGGACCTCGAAGCGCTCTGGGATGCCAA 600
 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 CGGGCTGGAAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCTTGCAGCCCGGGT 660
 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 GCGAGGAGGCGCGGGGCGAGTGCAGCGCAAGTCTGCCCTTGGCCAGAGGCGCAGCGCT 720
 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 GCGCTGCCCTGAGCCGAGCGGACGCGCGCTTGGGCGAGGGTCTCTGGGCGCCCGGGC 780
 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
 AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTACCTGCCAGACCGCGCAA 840
 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
 GAAGCCACCTCTTTGGAGGGTGGCTCTCTGGCACGCGCCACTCCACCCATCCGTGGGC 900
 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 CGCCAGCACCCGCGGGCGCGCCATCCACATCGCGGCCACCGCTCCCTGGGACACGCT 960
 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
 TGTCCCCGGGTACGCGGAGACCAAGCACTTCCTCTACTCTCAGGCGACAAGGAGCAG 1020
 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
 CTGCGGCGCTCCTTCTACTCAGCTCTCTGAGGCGCGAGCTGACTGGCGCTCGGAGGCTC 1080
 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 GTGGAGACCATCTTTCTGGGTTCCAGGCGCTGGATGCCAGGCACTCCCGCAGGTTGCC 1140
 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
 CGCTGCCCCAGCGCTACTGGCAATGCGGCGCGCTGTTCTGGAGCTGCTGGGAACAC 1200

FIG. 110

ASU	suPheLeuGluLeuLeuGlyAsnHis	4
	GCGCAGTGGCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTACCC	1260
	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
	CCAGCAGCCGGTGTCTGTGCCCGGAGAACGCCAGGGCTCTGTGGCGGCCCCGAGGAG	1320
	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
	GAGGACACAGACCCCGTCCGCTGGTGCACTGCTCCGCCAGCACAGACCCCTGGCAG	1380
	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
	GTGTACGGCTTCGTGGGGCTGCTCCGCCGGCTGGTCCCCAGGCTCTGGGGCTCC	1440
	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
	AGGCACAACGAACCGCTTCTCAGGAACACCAAGAAGTTCTCTCCCTGGGGAAGCAT	1500
	ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
	GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCTGCGGGCTGCGCTTGGCTG	1560
	AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
	CGCAGGAGCCAGGGGTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC	1620
	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
	CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTTC	1680
	LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	560
1	TTTTATGTACGGAGACCACTTTCAAAGAAGAGGCTCTTTTCTACCGGAAGAGTGTG	1740
2	PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
3	TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCACTGCGGGAG	1800
4	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
5	CTGTCCGAAGCAGAGGTGAGGCAGCATCGGGAAGCCAGGCCCCCTGCTGACGTCCAGA	1860
6	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
7	CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCGGATTGTGAACATGGACTACGTGCTG	1920
8	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
9	GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTGAGGGTGAAGGCA	1980
10	GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
11	CTGTTACAGCTGCTCAACTACGAGCGGGCGCGGCGCGCGCTCTGGGCGCTCTGTG	2040
12	LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
13	CTGGGCTGGACGATATCCACAGGGCTGGCGCACCTTCCTGCTGCTGTGCGGGCCCG	2100
14	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
15	GACCGCGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACCATC	2160
16	AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
17	CCCCAGACAGGCTCACGGAGGTGATCGCCAGCATCATCAACCCGAGAACACGTACTGC	2220
18	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	740
19	GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCTTCAAG	2280
20	ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
21	AGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCACAGTTCGTGGCTCACCTG	2340
22	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	780
23	CAGGAGACCAGCCCGTGAGGGATGCCGTCTCATCGAGCAGAGCTCTCCCTGAATGAG	2400
24	GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	800
25	GCCAGCAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCGTGCGCATC	2460
26	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
27	AGGGGCAAGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTG	2520
28	ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
29	CTCTGCAGCTGTGTACGGCGACATGGAGAACAGCTGTTTCCGGGGATTCCGGCGGAC	2580

FIG. 11P

GGGCTGCTCCTGCGTTTGGTGGATGATTCTTGTGGTGACACCTCACCTCACCCACGG 2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
AAAACTTCCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG 2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
CGGAAGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT 2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
CAGATGCCGGCCACGGCCTATTCCCTGGTGGCGCTGCTGCTGGATACCCGGACCCCTG 2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu 940
GAGGTGCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTC 2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
AACC CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG 2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
AAGTGTACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC 3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA 3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
TTTCATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCC 3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
TCCCTCTGCTACTCCATCCTGAAAGCCAGAACGAGGGATGTGCTGGGGCCCAAGGGC 3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
GCCCGCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC 3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAG 3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
ACG CAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGAGCCAAC 3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn 1120
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC 3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132

FIG. 11Q

[illegible]

FIG. 11R

[illegible]

FIG. 11S

[illegible]

FIG. 11T

AACTACTGATATATATGAGTTTTCAGTTTTCGA

ATGCTTGTATACAGGAGGAGGACCTGCACTTGGATGGGGTCCCTGTGG...AAATTTGGGGGAGGTGCTGTGGAGTAA

00500493 004100

FIG. 11U

[illegible]

FIG. 11V

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

FIG. 11W

00502490-001000

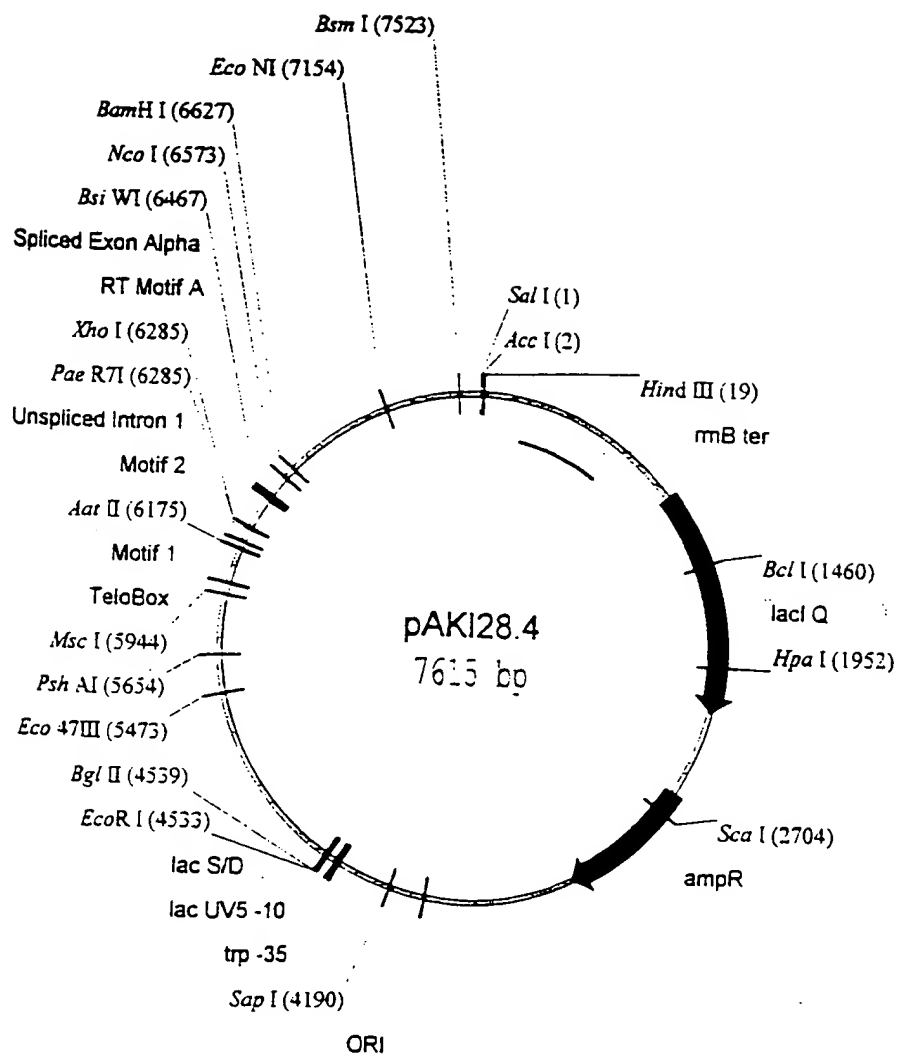


FIG. 13A

[illegible]

LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out

1	tcgacctgca	ggcatgcaag	cttggcactg	gcctgcgttt	tacaacgtcg	tgactgggaa
61	aacctctggcg	ttacceaaact	taatcgccct	gcagcacatc	cccccttcgc	cagctggcggt
121	ataatgcgaag	agggcccgac	cgatcgccct	tcccaacagt	tgcgcagcct	gaatggcgaa
181	tggcgctga	tgcggtattt	tctctctacg	catctgtgcg	gtatttcaca	ccgcataaat
241	tccctgtttt	ggcggtatgc	agaagatttt	cagctcgata	cagattaaat	cagaacgcag
301	aagcggcttcg	ataaaacaga	atttgccctg	cggcagtaga	gcgggtgtcc	cacctgcacc
361	catgccgaac	tcagaagtga	aacgccgatg	cgccgatgtg	agtggtgggt	ctccccatgc
421	gagatgaggg	aactcgccag	catcaataaa	aacgaaaggc	tcagtcgaaa	gactggggct
481	ttcggttttat	ctgttgtttg	tcggtgaacg	ctctcctgag	taggacaaat	ccgcggggag
541	cggatttcgaa	cgttgcgaag	caacggcccg	gaggggtggc	ggcagcagcg	ccgccataaa
601	ctgcacggca	tcaaaattag	cagaaggcca	tcctgacgga	tggccttttt	gcgtttctac
661	aaactcttcc	tgcgtctata	ctataagcc	atccccccac	agatacggta	aactagctat
721	gtttttgcat	caggaaagca	gggaatttat	ggtgcactct	cagtaacaat	tgctctgctg
781	ccgcatagtt	aagccagccc	cgacacccgc	caacacccgc	tgacgcgccc	tgacgggctt

FIG. 13B

SEQUENCE: 004100

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841 gtctgtctccc ggcatccgct tacagacaag ctgtgaccgt ctccgggagc tgcattgtgtc
901 agagggttttc accgtcatca ccgaaacgcg cgagacgaaa gggcctcgtg atacgcctat
961 ttttataggt taatgtcatg ataataatgg tttcttagac gtgaggttct gtacccgaca
1021 ccattcgaatg gtgcaaaaacc tttcgcggtg tggcatgata gcgcccgaa gagagtcaat
1081 tcagggtggt gaattgtgaaa ccagtaacgt tatacgatgt cgcagagtat gccggtgtct
1141 cttatcagac cgtttcccggt gtggtgaacc aggccagcca cgtttctgcy aaaacgcggg
1201 aaaaagtggg agcggcgatg gcggagctga attacattcc caaccgcgtg gcacaacaac
1261 tggcgggcaa acagtctgtg ctgattggcg ttgccacctc cagtctggcc ctgcacgcgc
1321 cgtcgcaaat tgtcgcggtg attaaatctc gcgcgatca actgggtgcc agcgtggtg
1381 tgtcgatggt agaacgaagc ggcgtcgaag cctgtaaagc ggcggtgcac aatcttctcg
1441 cgcaacgcgt cagtgggctg atcattaaact atccgctgga tgaccaggat gccattgtctg
1501 tgggaagctgc ctgcactaat gtcccggtgt tatttcttga tgtctctgac cagacaccca
1561 tcaacagtat tatttctctc catgaagacg gtacgcgact ggcgtgagc aatctgtctg
1621 cattgggtca ccagcaaatc gcgctgttag cgggccattt aagttctgtc tcggcgcttc
1681 tgcgtctggc tggctggcat aaatatctca ctccgaatca aattcagccg atagcggaac
1741 gggaaaggcga ctggagtgc atgtccggtt ttcaacaac catgcaaatg ctgaatgagg
1801 gcatcgttcc cactcgcatg ctgggtgcca acgatcagat ggcgtgggc gcaatgcgcg
1861 ccattaccga gtccgggctg cgcgttgggt cggatatctc ggtagtggga tacgacgata
1921 ccgaagacag ctccatgttat atcccgccgt taaccacat caaacaggat tttcgcctgc
1981 tggggcaaac cagcgtggac cgttgcgtgc aactctctca gggccagcg gtgaagggca
2041 atcagctgtt gcccgctctca ctggtgaaaa gaaaaaccac cctggcgccc aatacgcaaa
2101 ccgctctccc ccgcgcgctg gcgataat caatgcagct ggcacgacag gtttccgac
2161 tggaaagcgg gcagtgagcg caacgcaatt aatgtaagt agctccactca ttaggcaccc
2221 caggctttac actttatgct tccgacctgc aagaacctca cgtcaggttg cactttctgg
2281 ggaatgtgc gcggaacccc tatctgttta ttttctaaa tacattcaaa tatgtatccg
2341 ctcatgagac aataacctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt
2401 attcaacatt tccgtgtcgc ccttatctcc ttttctcggc catcttgcc tctgtctctt
2461 gctcaccag aaacgctggt gaaagtataa gatgctgaag atcagttggg tgcacgagtg
2521 ggttacatcg agaactggat ctcaacagcg gtaagatctt tgagagttct cgcgccgaag
2581 aacgtttctc aatgatgagc acttttaaa tctgtctatg tggcgcgcta ttatccgta
2641 ttgacgcgg gcaagagcaa ctccgttccc gcatacacta ttctcagaat gacttggttg
2701 agtactcacc agtcacagaa aagcatctta cggatggcat gacagtgaag gaattatgca
2761 gtgctgccat aacctgagt gatcaacctg cggccaactt actctgaca acgatcggag
2821 gaccgaagga gctaacggct tttttgcaca acatggggga tcatgtaact cgccttgatc
2981 gttgggaacc ggaactgaa gaaacctac caaacgacga gcgtgacacc acgatgcctg
2941 tagcaatggc aacaacgctg cgcgaactat taactggcga actacttact ctagcttccc
3001 ggcaacaatt aatagactgg atggaggcgg ataaagtctg aggaccactt ctgcgctcgg
3061 cctttccggc tggctggctt attgtgata aatctggagc cgttgagcgt gggctctcgcg
3121 gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagt atctacacga
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4141 ccgctcgcg cagccgaacg accgagcgca gcgagtcagt gagcagggaa gcggaagagc
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```

FIG. 13C

CGSC01493.001.000

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4381 aaggcgcaat cccgttcttg ataattgttt ttgcgccgac atcataacgg ttctggcaaa
4441 tattctgaaa tgagctgttg acaattaatc atcggctcgt ataattgttg gaattgtgag
4501 cggataacaa ttccacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
4561 tggcccgagt gctgcagagg ctgtgagcgc gcggcgcgaa gaacgtgttg gcttctggct
4621 tgcgctgctt ggacggggcc cgcgggggccc ccccgaggc cttcaccacc agcgtgcgca
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5341 tgcggccctt cttctactc agcttcttga gggccagctt gactggcgct cggaggctcg
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7141 aagatctctt tgcgtcaggg gtacaggttt cagcgaatgt tgcgtcagct cccatttcat
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7441 tctctctcag ggtatgtctt gggggccaa ggcgcgcgc gctctctgct cctcagggcc
7501 gtgcagtgct tgtgtccaca agcatctctt ctcaagctga ctgcacaccg tctcactac
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FIG. 13D

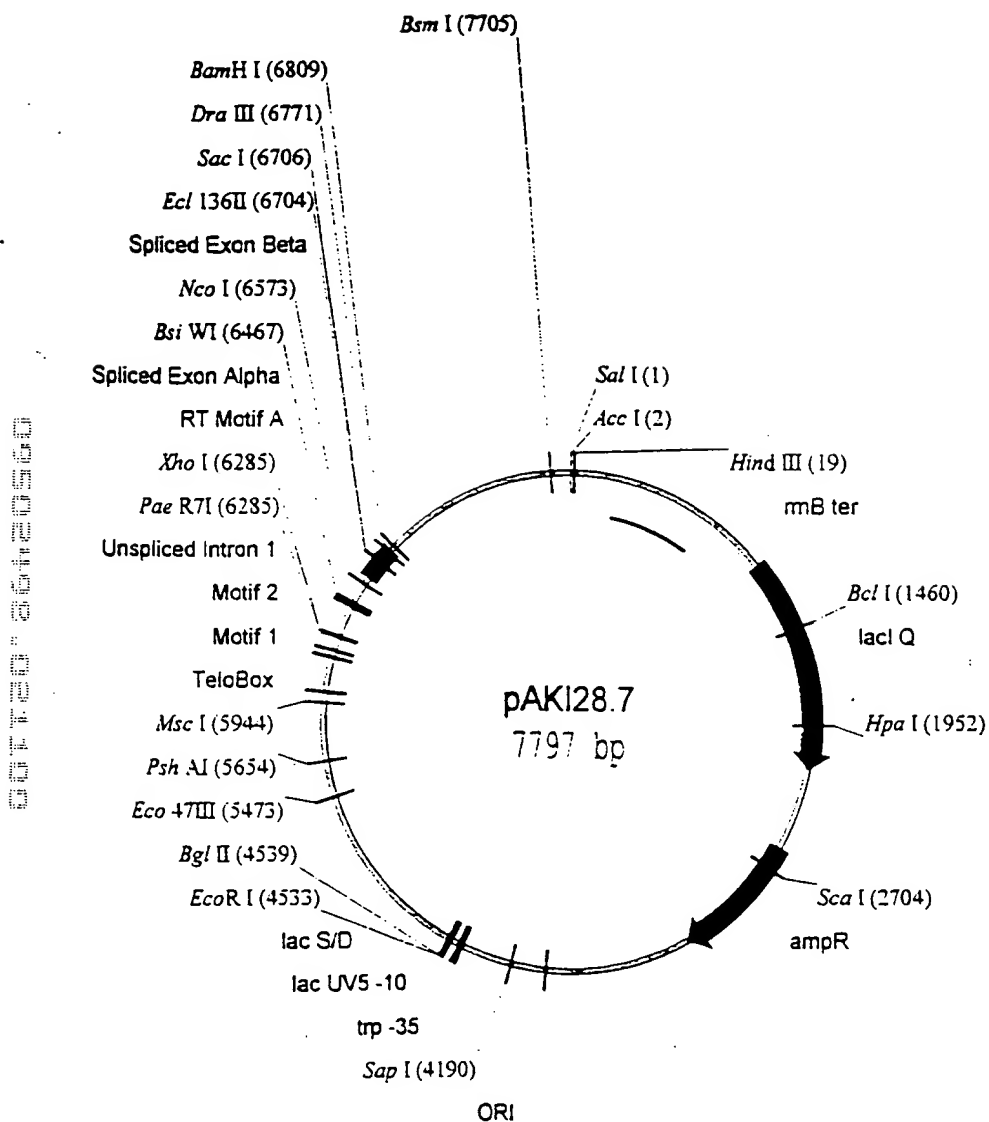


FIG. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

1 tcgacctgca ggcattgcaag ctctggcactg gccctgcgttt tacaacgtcg tgactgggaa
61 aacctctggcg ttacccaact taatcgccctt gcagcacatc cccctttcgc cagctggcgct
121 aatagcgaag aggcccgac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
181 tggcgcgctga tgcggtattt tctccttacg catctgtgcg gtatttcaca ccgcataaat
241 tcctcgtttt ggcggattgag agaagatttt cagcctgata cagattaaat cagaacgcag
301 aagcgtgtctg ataaaacaga attgccctg cgccagtatgc gcggtggctc cacctgacct
361 catgccgaac tcagaagtga aacgccgtag cgcgcatggt agtgtggggg ctccccatgc
421 gagagtaggg aactgccagg catcaataa aacgaaaggc tcagtgcgaaa gactgggcct
481 ttcgttttat ctgtttgtttg tcggtgaacg ctctcctgag taggacaaat ccgcggggag

FIG. 14B

FIG. 14C

PRINT OF DRAWINGS
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3961 tctgacttga gctgctgatt ttgtgatgct cgtcaggggg ggggagccta tggaaaaacg
4021 ccagcaacgc ggccttttta cgggttcttg ccttttctg gccttttct cactgttct
4081 ttctctgctt atcccttgat tctgtggata accgtattac cgcctttgag tgagctgata
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4681 gctacctgct caacacgggt accgacgcac tgcgggggag cggggcgctg gggctgctgc
4741 tgcgctgctt gggcgacgac gtgtctggtt accgtctggc acgctgcgct cctcttctgc
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6361 tgggcttggg cgtatctaac agggcttggc gcactctgt gctgctgtgt cggggccagg
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FIG. 14D

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FIG. 14E

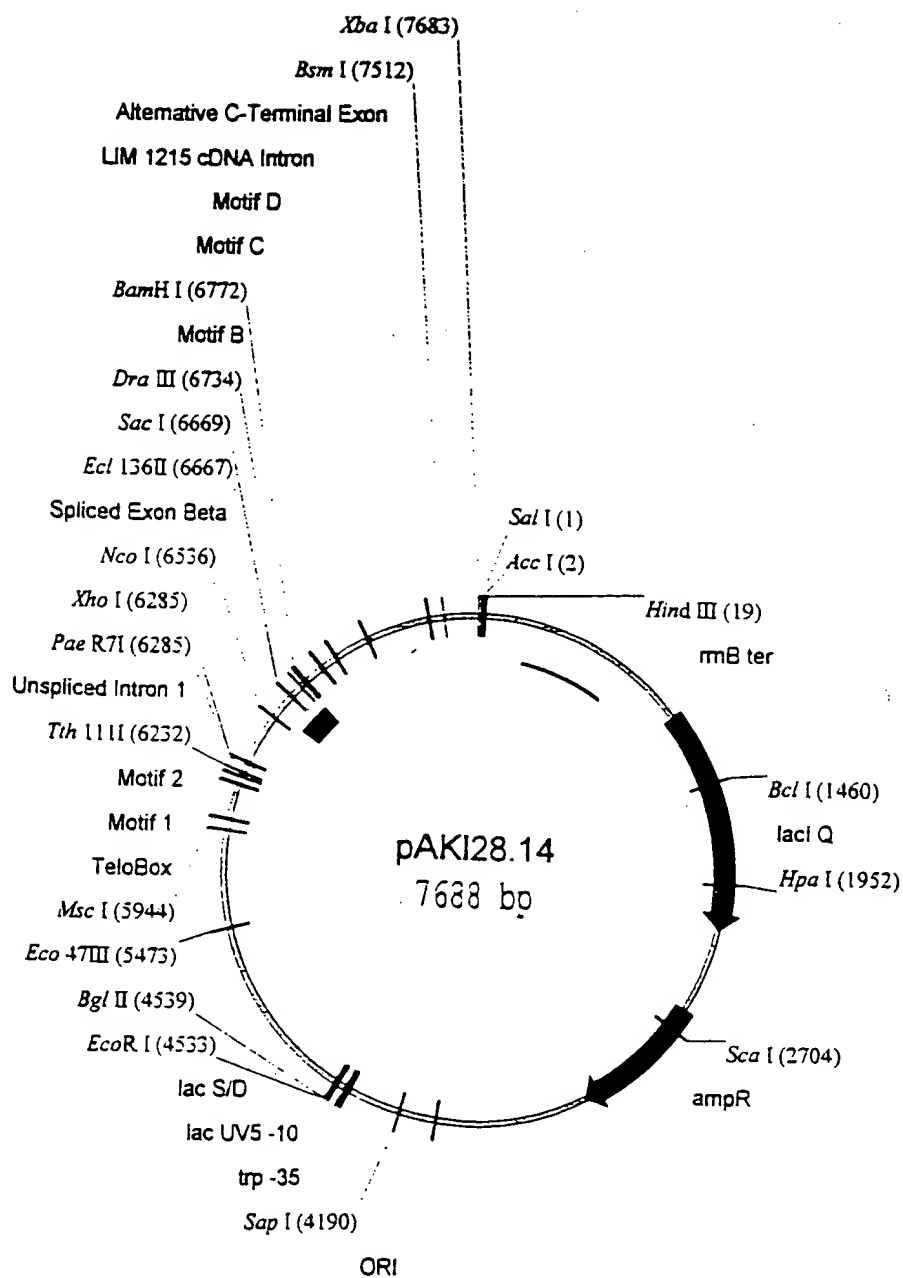


FIG. 15A

PRINT OF DRAWINGS
AS ORIGINALLY FILED

LOCUS pAK129.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

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61 aaccctggcg ttacccaact taatcgctt gcagcacatc cccctttcgc cagctggcgt
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541 cggatttgaa cgttgcgaag caacggcccg gaggggtggcg ggaggagcgc ccgccataaa
601 ctgccaggca tcaaatatag cagaaggcca tccctgacgga tggccttttt gcgtttctac
661 aaactcttcc tgcgtccta tctacaagcc atccccccac agatacggta aactagcctc
721 gtttttgcac caggaaagca gggaatttat ggtgcactct cagtacaaat tgctctgatg
781 ccgcataagt aagccagccc cgacacccgc caacacccgc tgacgcgccc tgacgggctt
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FIG. 15B

3361 aaatccctta acgtgagttt tegtccact gagcgtcaga ccccgtagaa aagatcaaa
3421 gatcttcttg agatcccttt tttctgcgag taatctgctg cttgcaaaaca aaaaaaccac
3481 cgctaccagc ggtggtttgt ttgcccagac aagagctacc aactcttttt ccgaaggtaa
3541 ctggcttcag cagagcgagc ataccaaata ctgtccctct agtgtagccg tagttaggcc
3601 accacttcaa gaactctgta gcaccgccta catacctcgc tctgtaatac ctgttaccag
3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttag
3721 cggataaggc gcagcgtctg ggcgaacgg ggggttcgtg cacacagccc agcttgagac
3781 gaacgacctt caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc
3841 ccgaaggag aaaggcgac aggtatccgg taagcggcag ggtcggaaaca ggagagcgca
3901 cgagggagct tccaggggga aacgcctggg atctttatag tctgtcggg tttcgccacc
3961 tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg gcggagccta tggaaaaacg
4021 ccagcaacgc ggccttttta cggcttctgg ccttttgctg gccttttgct cacatgttct
4081 tttctgcgtt atccctgat tctgtgata accgtattac cgcttttgag ttagctgata
4141 ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa cggaagagc
4201 gcccaatcag caaacgcctt cttcccgcg cttggccgat tcattaatgc agaattaatt
4261 ctcatgtttg acagcttatt atcgactgca cgggtgacca atgtctctgg cgtcagcgag
4321 ccatcggaag ctgtggtatg gctgtgagg tctgaaatca ctgcataatt cgtgtcgtct
4381 aaggcgcact cccgttctgg ataatgtttt ttgcccagac atcataacgg tttcgcaaa
4441 tatcttgaaa tgagctgttg acaattaatc atcggctcgt ataattgttg gaattgttag
4501 cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg
4561 tggcccgagc gctgcagagg ctgtgcagc gcggcgcgaa gaacgtgctg gccctcgcc
4621 tgcgctgctt ggacggggcc cgggggggccc ccccgaggcc cttcaccacc agcgtcgca
4681 gctacctgct caacacgggt accgacgctac tgcgggggag cggggcgctg gggctgctgc
4741 tgcgcgctg gggcgacgac gttgtgtgtt acctgctggc agctgctggc cttctgtgct
4801 tgggtgctcc cagctgcgct taccaggtgt gggggcgccc gctgtaccag ctcggcgctg
4861 ccactcaggc cggggccccc ccacacgcta gtggaccccg aaggcgctct ggatcggaac
4921 gggccctgaa ccatagcgtt agggagggcg gggctccccc gggcctgcca gccccgggtg
4981 cgaggagggc cgggggcagc gctcagcgaa gtctgcgctt gcccaagagg cccagcgctg
5041 gcgctgcccc tgagcgggag cggacgcccc ttgggcaggg gtccctgggc caccgggga
5101 ggacgctgtg accgagctac cgtgtgtttt gtgtgtgttc acctgccaag ccccggaag
5161 aagccacctt tttggagggt ggccttcttg gcacgcgcca ctccaccca tccgtgggc
5221 gccagcaca cgcggggccc ccatcccat cggcgccacc acgtccctgg gacacgctt
5281 gtcccccgtt gtacgctgag accaagcact tctctactc ctcaggcgag aaggagcagc
5341 tgcggccccc cttctacttc agctctctga ggcaccagct gactcgctcg cggaggtctg
5401 tggagacctt cttctgtgtt tccagggccc ggaatgccag gactccccgc aggtcgccc
5461 gccctgcccc gcgtacttg caaatgtggc cctctgtctt ggagctgctt gggaaaccag
5521 cgcagtgccc ctacgggggt cttctcaaga cgcactgccc gctgcgagct gcggccacc
5581 cagcagcggg tgtctgtgct cggggaagc cccagggctt tgtggcgccc cccgagggag
5641 aggacacaga ccccgctcgc ctgtgtcagc tgcctcgcca gcacagcagc ccttgccag
5701 tgtacggctt cgtgcggggt tgcctgcgct ggcctgtgct cccagggctt tggggctcca
5761 ggcacaacga acccgcttct ctcagggaaca ccaagaagt catctccctg gggaaagcatg
5821 ccaagcttct gctgcaggag ctgacgttga agatgagcgt gcgggactgc gcttgctgc
5881 gcaggagccc aggggttgcc tgtgtctcgg ccgcagagca cgtctgtcgt gaggagatcc
5941 tggccaagt cctgcactgg ctgtatgagt tgtacgtcgt ctagctgctc aggtcttct
6001 tttatgtcac ggaagccacg tttcaaaaga acaggctctt tttctaccgg aagagtgtct
6061 ggaagcaagt gcaaaagcat ggaattagac agcacttgaa gaggtgagc ctgcgggagc
6121 tgtcggaagc agaggttagg cagcatctgg aagccaggcc cgcctctgct acgtccagac
6181 tccgcttcat ccccaagcct gacgggctgc ggcgaattgt gaacatggac tacgtcgtgg
6241 gagccagaac gttccgcaga gaaaagagg ccgagcgtct cacttcgagg gtgaaggcac
6301 tgttcagcgt gctcaactac gacgggctgc ggcggcccg cctcctgggc gcctctgtgc
6361 tgggctggga cgatatccac agggctctgc gcacctctg gctgcgtgtg cggggccagg
6421 acccgccgct tgagctgtac tttgtcaagg acaggctcac ggaggtcatc gccagcatca
6481 tcaaacccag aacacgtact gctgtcgtct gtaagcgtg gtccagaagg ccgccatgg
6541 gcacgtccgc aaggccttca agagccact cttctacctg acagacctcc agcgtacat
6601 gcagagcttc gtggctcacc tgcaggagac cagcccgctg agggatggcg tctcatcga
6661 gcagagcttc tccctgaatg aggcagcag tggcctcttc gacgtcttcc tacgttcat
6721 gtgcccacc gccgtgcgca tcaaggcgaa gtctacgtc cagtgcagg ggaatccgca

FIG. 15C

6781 gggtccatc ctctccacgc tgctctgcag cctgtgctac ggcgacatgg agaacaagct
6841 gtttgcgggg attcggcggg acgggctgct cctgcgtttg gtggatgatt tcttggtggg
6901 gacacctcac ctcacccacg cgaaaacctt cctcaggacc ctgggtccgag gtgtccctga
6961 gtatggctgc gtggtgaact tgcggaagac agtgggtaac ttccctgtag aagacgaggc
7021 cctgggtggc acggcttttg ttcagatgcc ggcccacggc ctattcccct ggtgcggcct
7081 gctgctggat acccgaccc tggagggtgca gagcgactac tccagctatg cccggacctc
7141 catcagagcc agtctcacct tcaaccgcgg cttcaaggct gggaggaaca tgcgtcgcaa
7201 actctttggg gtcttgcggc tgaagtgtca cagcctgttt ctggatttgc aggtgaacag
7261 cctccagacg gtgtgcacca acatctacaa gatcctcctg ctgcaggcgt acagggttca
7321 cgcatgtgtg ctgcagctcc catttcatca gcaagtttgg aagaaccca catttttct
7381 gcgcgtcatc tctgacacgg cctcccctctg ctactccatc ctgaaagcca agaacgcagg
7441 gatgtcgctg ggggcccaagg gcgcgcgcgg ccctctgccc tccgaggccg tgcagtggct
7501 gtgccaccaa gcattcctgc tcaagctgac tcgacaccgt gtcacctacg tgccactcct
7561 ggggtcactc aggacagccc agacgcagct gagtcggaag ctcccgggga cgacgtgac
7621 tgccctggag gccgcagcca acccggcact gccctcagac ttcaagacca tcttgactg
7681 atctagag

CGCCTGAG

FIG. 15D